Amendments to the Specification:

Please replace the paragraph commencing at page 26, line 27, with the following amended paragraph:

The term "physiological conditions" is used herein in two meanings. With reference to culturing cells or the like, it means an extracellular milieu having conditions (e.g., temperature, pH, and osmolarity) which allows for the sustenance or growth of a cell of interest. With reference to the ~~the~~ species of secretory component (SC) which is most abundant under such conditions, "physiological conditions" refers to the conditions normally present in the organ of interest or tissue of interest, such as the lumen of the small or large intestine.

Please replace the paragraph commencing at page 30, line 14, with the following amended paragraph:

The nucleic acid and amino acid sequence of the polymeric immunoglobulin receptor has been identified in a variety of taxonomically diverse species. *See*, Piskurich *et al.*, *Journal of Immunology* 154:1735-1747 (1995). The sequence of human pIgR is set forth, *inter alia*, in Eiffert et al., Hoppe Seyler's Z. Physiol. Chem. Bd. 365, S.1489-1495 (1984), and in Hughes et al., FEBS Letters 410:443-446 (1997), and further set forth in SWISS-PROT, a curated protein sequence database maintained by the European Molecular Biology Laboratory Data Library, under accession number P01833 (the sequence is publicly available on the World Wide Web at, e.g., ~~www.~~expasy.ch/cgi-bin/sprot-search-ac?P01833). The numbering in SWISS-PROT (see, e.g., SEQ ID NO:1) includes an 18-residue leader sequence; thus, references to particular residues in the SWISS-PROT database are 18 numbers higher than the numbers accorded the same residues by references which do not include the leader sequence (such as Hughes et al. and the Mostov and Kaetzel reference), even though they refer to the same protein. References herein to one or more numbered residues of human pIgR are to the residues as

numbered in the SWISS-PROT database. The SWISS-PROT database also reports that an alanine to valine variant has been found at position 580 of the sequence. Ligands that bind to B regions containing this or other similar variants are encompassed within the present invention. Such variants include variants of the sequence set forth in SWISS-PROT so long as they do not destroy the function of the variant pIgR molecule as a receptor for polymeric immunoglobulin and do not destroy the ability of the variant pIgR molecule to internalize and transcytose a ligand bound to it. Assays for determining internalization and transcytosis of a bound ligand are set forth in the Examples.

Please replace the paragraph commencing at page 34, line 22, with the following amended paragraph:

Sequences of pIgR from different species can be aligned, as in Figure 1. It should be noted that Figure 1 employs various gaps and insertions to align the sequences of the different species and the numbering used is a "unified" numbering that does not correspond to any one species. The sequence of human pIgR is set forth, *inter alia*, in Eiffert et al., *supra*, and in Hughes et al., *supra*, and further set forth in SWISS-PROT, a curated protein sequence database maintained by the European Molecular Biology Laboratory Data Library, under accession number P01833 (the sequence is set forth herein as Figure 2 and is publicly available on the World Wide Web at, e.g., ~~www.~~expasy.ch/cgi-bin/sprot-search-ac?P01833). The numbering in SWISS-PROT includes the 18-residue leader sequence shown in Figure 1; thus, references to particular residues in the SWISS-PROT database are 18 numbers higher than the numbers accorded the same residues by references which do not include the leader sequence (such as Hughes et al.), even though they refer to the same protein. References below to one or more numbered residues of human pIgR are to the residues as numbered in the SWISS-PROT database.